

REMARKS

Entry of the foregoing, reexamination and reconsideration of the above-identified application is respectfully requested.

New claims 28-34 have been added, directed to preferred embodiments of the invention. Support for new claims 28-30 is found at the very least on page 7, lines 29-35. Support for new claims 31-34 may be found at the very least at page 7, line 36 - page 8, line 33.

The disclosure has been objected to as containing an embedded hyperlink and/or other form of browser-executable code. The specification has been amended at page 13 to delete the link and instead provide a reference describing the program used. By going to the link, the information now set forth in the specification was obtained. No new matter is thus added by this amendment.

Claims 1-3, 7-10, 12-22 and 24-27 have been rejected under 35 U.S.C. §112, second paragraph, as allegedly being indefinite. This rejection has been traversed in part and rendered moot in part by the instant amendment.

Claim 1 and other claims having the same language are asserted to be indefinite in the recitation of "gene." The claims have been amended, as helpfully suggest by the Examiner, to recite a "polynucleotide."

It is further asserted that it is unclear if the gene or the amino acid sequence is involved in the differentiation and has a homeodomain-like sequence. Applicants note that this language has been deleted from claim 1 as it is not necessary to define the claimed

polynucleotide. However, this language would be sufficiently clear to a person skilled in the art based upon the specification as filed. By reference to the specification, it is clear that it is the protein that has the claimed properties. The relevant claims have been amended, as helpfully suggested by the Examiner, to recite “wherein said protein” is involved in the differentiation and has a homeodomain-like sequence.

The Official Action further alleges that the terms “involved” and “homeodomain-like” are indefinite since the metes and bounds cannot be determined and the terms are not defined in the specification. This assertion is in error. Applicants note that the specification states at page 5, lines 21-30:

As used herein, a protein that is involved in differentiation and that has a homeodomain-like sequence is a protein that is involved in the process in which cells differentiate into morphologically and/or functionally different cells such as differentiation into adventitious shoots, branches, leaves, flowers or the like, and that has a homeodomain-like sequence functioning as a DNA-binding domain, and specifically a protein that induces the formation of adventitious shoots, a protein that induces branching, and the like.

“Homeodomain” is also defined in the specification at page 2, lines 2-6, as a “61 amino acid sequence translated from [the homeobox] region” and as having “a helix-turn-helix structure comprising three α helices and which recognizes a specific nucleotide sequence thereby to bind DNA.” This description in combination with that at page 5 quoted above, shows that the homeodomain-like sequence provides a DNA-binding domain.

“Homeodomain” and “homeobox” sequences are also well known in the art, as shown by the references cited during prosecution of the instant application.

“Homeodomain-like” is thus sufficiently definite when read by a person skilled in the art in light of the specification.

In claim 7, it is allegedly unclear what conditions are required for a protein to “have an ability.” The Examiner helpfully suggests amending the claim to delete this recitation and instead recite “wherein said protein induces ...” A similar amendment is suggested for claim 13. In claims 16, 25 and 26, the word “from” should be replaced with “in,” and the word “in” should be inserted after the first “or.” In claim 16, the metes and bounds of “driving the expression of” cannot be determined. The Examiner helpfully suggests amending the claim to instead recite “transcribing.” These suggested amendments have been incorporated into the claims, with the exception of “in” after the first “or.” That recitation is believed to be unnecessary. By the use of “or,” it is implicit that the differentiation is “in” *either* a plant or a plant cell. The second “in” is unnecessary.

In view of the amendments, withdrawal of this rejection is respectfully requested and believed to be in order.

Claims 16 and 25 are also rejected under §112, second paragraph, as allegedly being incomplete for omitting essential steps. This rejection is now moot in view of the instant amendment.

The alleged omitted step is “wherein the expression of said gene induces differentiation in a plant or in a plant cell.” Claims 17 and 26 are also rejected under §112, second paragraph, as allegedly being incomplete for omitting essential steps. The alleged omitted step is “wherein the expression of said gene induces adventitious shoot

formation in a plant.” Similarly, claims 18 and 27 are rejected under §112, second paragraph, as allegedly being incomplete for omitting essential steps. The alleged omitted step is “wherein the expression of said gene induces branching in a plant.” The suggested language has been added to each of the claims. These amendments do not narrow their scope, but instead the claims now recite in the body of the claim what is implicit based upon the preamble.

Claims 17 and 26 are also said to be indefinite for the recitation of “or a plant cell” since it is asserted to be physiologically impossible for a “plant cell” to form adventitious shoots. Deletion of “or a plant cell” was suggested, and has been done.

In view of the instant amendments, withdrawal of the rejection of record is respectfully requested.

Claims 2, 3, 18-22 and 25-27 have been rejected under 35 U.S.C. §112, first paragraph, as allegedly not being enabled by the specification. This rejection is respectfully traversed.

The Official Action acknowledges that the specification enables claims directed to a polynucleotide encoding a protein whose amino acid sequence is SEQ ID NO:2, as well as vectors, transformed host cells, plant and plant cells, and methods for inducing adventitious shoot formation and branching. However, it is asserted that claims drawn to a method of inducing differentiation using the above nucleic acid sequence and claims wherein the sequence of SEQ ID NO:2 is modified by addition, deletion and/or

replacement, and methods of inducing differentiation, adventitious shoot formation and branching using such a modified sequence, are not enabled.

According to the Official Action, it cannot be predicted by one skilled in the art that nucleic acids having a modified sequence will encode a protein having the same activity as SEQ ID NO:2. The Examiner further asserts that while the claims are drawn to nucleic acid sequences that hybridize to SEQ ID NO:1, there is no guidance for selecting sequences that encode a protein whose function is the same as the encoded protein of SEQ ID NO:2. It allegedly would be unpredictable whether any of the encoded proteins will induce adventitious shoot formation and branching when transformed into a plant. Undue experimentation to generate plants with induced adventitious shoot formation and branching would thus be required.

It is respectfully submitted that one skilled in the art, reading the claims in light of the specification, would be enabled to practice the invention as claimed. With respect to claim 2, one skilled in the art could readily make modifications to the amino acid sequence and screen the protein to determine whether or not it retains the recited activity. With respect to claim 3, one skilled in the art could screen the proteins which hybridize and determine whether the encoded protein has the recited activity. Since the hybridization is under stringent conditions, the number of proteins to be screened would not be unduly high and no undue burden would exist for screening them. By following the Examples in the specification, one skilled in the art could screen to determine whether the obtained sequences have the required activity.

Moreover, new claims 28-34 limit the scope of polynucleotides being claimed by limiting the number of amino acids to be modified, requiring the hybridizing DNA to have a length of 75% or greater of the entire sequence of SEQ ID NO: 1 and include a part or all of the homeodomain sequence, and requiring a high degree of homology between the sequences. Since the number of polynucleotides is thus limited, in particular, no undue experimentation would be required to screen species to determine whether they fall within the scope of these claimed. These new claims are in particular fully enabled.

With respect to the method for inducing differentiation, differentiation is said to encompass all aspects of plant development including root growth, leaf development and flower development. The claims have been amended in keeping with the statement in the Official Action, acknowledging that the instant specification describes and enables adventitious shoot formation and branching, so that the "differentiation" is selected from these two types.

In view of the above, withdrawal of the rejection of record is respectfully requested. Such action is believed to be in order.

Claims 2, 3, 19-22 and 24-27 have been rejected under 35 U.S.C. §112, first paragraph, as allegedly containing subject matter not described in the specification. This rejection is respectfully traversed.

According to the Official Action, the specification only discloses the nucleic acid sequence of SEQ ID NO: 1 encoding SEQ ID NO:2, and does not disclose any specific structural, physical and/or chemical properties for the modified claimed sequences. It is

asserted that the specification does not describe a homeodomain or a homeodomain-like sequence, and that it “is unclear if all proteins exhibiting a homeodomain-like sequence will exhibit the recited function.” It is concluded that applicants were not in possession of the modified sequence(s) that would hybridize to SEQ ID NO:1 under unspecified or low stringency conditions.

These assertions and conclusions are in error. In Example 3, the M6 clone was obtained and its nucleotide sequence determined, which is SEQ ID NO: 1. The corresponding amino acid sequence is SEQ ID NO: 2. Example 3 further provides:

During the course of cloning, a cDNA clone of a sequence that had an identity of 86% within the homeodomain and 40% in the entire region with MSH cDNA was isolated and was designated M8. The nucleotide sequence is shown in SEQ ID NO: 3 of the sequence listing, and the corresponding amino acid sequence is shown in SEQ ID NO: 4.

In Example 4, the mutant overexpressing the MSHM8 cDNA was shown to have more branching. The instant application thus does show a modified sequence and sequence which would hybridize that has the required activity. Applicants indeed had possession of the invention as recited in the claims.

Withdrawal of the rejection of record is thus respectfully requested and believed to be in order.

Claims 1-3 have also been rejected under 35 U.S.C. §101 as being directed to non-statutory subject matter. This rejection has been rendered moot by the instant amendment.

The claims have been amended to recite “isolated,” as suggested by the Examiner, to overcome this rejection.

Withdrawal of this rejection is thus respectfully requested and believed to be in order.

Claims 2, 3, 20-22, 24, 25 and 27 have been rejected under 35 U.S.C. §102(b) as allegedly being anticipated by Uberlacker et al (1994). This rejection is respectfully traversed.

Uberlacker et al (1994) is said to teach a maize homeobox gene Zmbox1b that, when transformed into tobacco, produce developmental abnormalities, including increased branching. The homeobox gene is said to inherently comprise a homeodomain-like sequence, which affects development and is thus inherently involved in differentiation. The sequence of Uberlacker et al would allegedly be produced by modifying the sequence of SEQ ID NO:2.

The claim as amended requires that the modified sequence have “at least 20% amino acid identity to SEQ ID NO: 2.” The sequence of Uberlacker et al (1994) does not share such a high degree of sequence identity. The sequence of Uberlacker et al has only about 15% identity with SEQ ID NO: 2.

Withdrawal of the rejection of record is thus respectfully requested and believed to be in order.

Claims 2, 3, 20-22, 24, 25 and 27 have been rejected under 35 U.S.C. §102(b) as allegedly being anticipated by Uberlacker et al (1996). This rejection is respectfully traversed.

Uberlacker et al (1996) is said to teach maize homeobox genes Zmbox1a and Zmbox1b that, when transformed into tobacco, produce developmental abnormalities, including adventitious shoots. The homeobox gene is said to inherently comprise a homeodomain-like sequence, which affects development and is thus inherently involved in differentiation. The sequences of Uberlacker et al would allegedly be produced by modifying the sequence of SEQ ID NO: 2.

The claim as amended requires that the modified sequences have “at least 20% amino acid identity to SEQ ID NO: 2.” The sequence of Uberlacker et al (1996) does not share such a high degree of sequence identity. The sequence of Uberlacker et al has only about 15% identity with SEQ ID NO: 2.

Withdrawal of the rejection of record is thus respectfully requested and believed to be in order.

Applicants note with appreciation the indication that SEQ ID NO: 1 encoding SEQ ID NO: 2 are free of the prior art. Claims limited to these sequences were thus stated to be allowable. In view of the instant amendments, all of the claims now of record are believed to be allowable.

In the event that there are any questions relating to this amendment or the application in general, it would be appreciated if the Examiner would contact the undersigned attorney at (650) 622-2360.

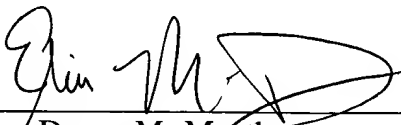
Further and favorable action in the form of a notice of allowance is respectfully
requested.

Respectfully submitted,

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